Applicant: Deryck J. Williams et al. Attorney's Docket No.: 12557-011001

Serial No.: 10/602,268 Filed: June 23, 2003

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Amendments to the Specification:

Please insert the paper copy of the Sequence Listing filed herewith following the Oath/Declaration.

Please replace the paragraph beginning at page 35, line 8, as with the following amended paragraph:

C. elegans can be grown on lawns of E. coli genetically engineered to produce doublestranded RNA (dsRNA) designed to inhibit PEAMT1 or PEAMT2 expression. Briefly, E. coli were transformed with genomic fragments encoding portions of the C. elegans PEAMT1 or the PEAMT2 gene. Specifically, a 960 nucleotide fragment was amplified from the PEAMT1 gene using oligo-nucleotide primers containing the sequences 5'-ATGGTGAACGTTCGTCGTGC-3' (SEQ ID NO:29) and 5'-CATACGTATTTCTCATCATC-3' (SEQ ID NO:30) respectively, or an 854 nucleotide fragment was amplified from the PEAMT2 gene using oligo-nucleotide primers containing the sequences 5'-CCAGATTATTACCAACGCCG-3' (SEQ ID NO:31) and 5'-TGAACTTACATAGATTCTTG-3' (SEQ ID NO:32) respectively. The PEAMT1 and PEAMT2 genomic fragments were cloned separately into an E. coli expression vector between opposing T7 polymerase promoters. The clone was then transformed into a strain of E. coli that carries an IPTG-inducible T7 polymerase. As a control, E. coli was transformed with a gene encoding the Green Fluorescent Protein (GFP). Feeding RNAi was initiated from C. elegans larvae at 23 °C on NGM plates containing IPTG and E. coli expressing the C. elegans PEAMT1 or PEAMT2, or GFP dsRNA. If the starting worm (the P0) was an L1, or a dauer larva, the phenotype of both the PEAMT1 and PEAMT2 RNAi-generated mutants was complete or almost complete sterility. One the other hand, if the P0 animal was an L4 larva, then the phenotype of both the PEAMT1 and PEAMT2 RNAi-generated mutants was L1/L2 larval arrested development and lethality. The sequence of the PEAMT1 and PEAMT2 genes is of sufficiently high complexity (i.e., unique) such that the RNAi is not likely to represent cross reactivity with other genes.